

SEQUENCE LISTING

<110> Crane, Edmund H.
Crane, Virginia C.

<120> Maize Pathogenesis-Related
Polynucleotide and Methods of Use

<130> 35718/214291

<150> US 60/195,801

<151> 2000-04-10

<160> 3

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 898

<212> DNA

<213> Zea mays

<220>

<221> CDS

<222> (63)...(674)

<400> 1

ctcgcacgca ctcgacgctc attcactgag ccatttactc agatcaccaa ctccagatct	60
ca atg gcg cac tcg cgc agc cac cac ctc ctc ctg ctc ccc gcg	107
Met Ala His Ser Arg Ser His His His Leu Leu Leu Leu Pro Ala	
1 5 10 15	

ccc atg gcc acg gcg tgc ttg ctc ctc gcc acc ctc ctc gcg ctc tgc	155
Pro Met Ala Thr Ala Cys Leu Leu Leu Ala Thr Leu Leu Ala Leu Cys	
20 25 30	

gcc gcg ccg gcg ccg acc cac ggc gcg cgc gtc ctc atg ccg ggc ggc	203
Ala Ala Pro Ala Pro Thr His Gly Ala Arg Val Leu Met Pro Gly Gly	
35 40 45	

gcg ggc gcg gtg acc aag gcg cag cag ggt ggc acc ggc agc ggc agc	251
Ala Gly Ala Val Thr Lys Ala Gln Gln Gly Gly Thr Gly Ser Gly Ser	
50 55 60	

aac gcg acg gcg gac gag tac ctg gcg ccg cac aac cag gcg cgc gcg	299
Asn Ala Thr Ala Asp Glu Tyr Leu Ala Pro His Asn Gln Ala Arg Ala	
65 70 75	

gcg gtg ggc gtg gcc ccg ctg cgg tgg aac gcg ggc ctg gct tcg gcg	347
Ala Val Gly Val Ala Pro Leu Arg Trp Asn Ala Gly Leu Ala Ser Ala	
80 85 90 95	

gcc gcg ggg acg gtg gcg cag cag cgg cgg cag ggc ggg tgc gcg ttc	395
Ala Ala Gly Thr Val Ala Gln Gln Arg Arg Gln Gly Gly Cys Ala Phe	
100 105 110	

gcg gac gtg ggg gcc agc ccc tac ggc gcg aac cag ggg tgg gcg agc 443
Ala Asp Val Gly Ala Ser Pro Tyr Gly Ala Asn Gln Gly Trp Ala Ser
115 120 125

tac cgc gcg cgc ccc gcc gag gtg gtg gcg ctg tgg gtg gcg gag ggg 491
Tyr Arg Ala Arg Pro Ala Glu Val Val Ala Leu Trp Val Ala Glu Gly
130 135 140

cgg tac tac acc cac gcc aac aac acg tgc gcc gcg ggg cgg cag tgc 539
Arg Tyr Tyr Thr His Ala Asn Asn Thr Cys Ala Ala Gly Arg Gln Cys
145 150 155

ggc acg tac acg cag gtg gtg tgg cgc aac acc gcc gag gtc ggg tgc 587
Gly Thr Tyr Thr Gln Val Val Trp Arg Asn Thr Ala Glu Val Gly Cys
160 165 170 175

gcg cag gcc agc tgc gcc acg ggc gcc acg ctc acg ctc tgc ctg tac 635
Ala Gln Ala Ser Cys Ala Thr Gly Ala Thr Leu Thr Leu Cys Leu Tyr
180 185 190

aac ccg cac ggc aac gtg cag ggc cag agc ccc tac tag ctagctgagg 684
Asn Pro His Gly Asn Val Gln Gly Gln Ser Pro Tyr *
195 200

tcatacaggtc gtagcgacgg agcccaactg ccgccgccgg cggcagcgga gtacgtaggt 744
tcatacagttc tctctagttc ggtcacggaa aggctgtttt gtgggtgtgat ccgggtggtg 804
tcttggtgtt gttgacaact gctttggttt ggtgtatcag cttttgttgc cgggtaaaaa 864
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 898

<210> 2

<211> 203

<212> PRT

<213> Zea mays

<400> 2

Met Ala His Ser Arg Ser His His His Leu Leu Leu Leu Pro Ala Pro
1 5 10 15
Met Ala Thr Ala Cys Leu Leu Leu Ala Thr Leu Leu Ala Leu Cys Ala
20 25 30
Ala Pro Ala Pro Thr His Gly Ala Arg Val Leu Met Pro Gly Gly Ala
35 40 45
Gly Ala Val Thr Lys Ala Gln Gln Gly Gly Thr Gly Ser Gly Ser Asn
50 55 60
Ala Thr Ala Asp Glu Tyr Leu Ala Pro His Asn Gln Ala Arg Ala Ala
65 70 75 80
Val Gly Val Ala Pro Leu Arg Trp Asn Ala Gly Leu Ala Ser Ala Ala
85 90 95
Ala Gly Thr Val Ala Gln Gln Arg Arg Gln Gly Gly Cys Ala Phe Ala
100 105 110
Asp Val Gly Ala Ser Pro Tyr Gly Ala Asn Gln Gly Trp Ala Ser Tyr
115 120 125
Arg Ala Arg Pro Ala Glu Val Val Ala Leu Trp Val Ala Glu Gly Arg
130 135 140
Tyr Tyr Thr His Ala Asn Asn Thr Cys Ala Ala Gly Arg Gln Cys Gly
145 150 155 160
Thr Tyr Thr Gln Val Val Trp Arg Asn Thr Ala Glu Val Gly Cys Ala
165 170 175

Gln Ala Ser Cys Ala Thr Gly Ala Thr Leu Thr Leu Cys Leu Tyr Asn
180 185 190
Pro His Gly Asn Val Gln Gly Gln Ser Pro Tyr
195 200

<210> 3
<211> 612
<212> DNA
<213> Zea mays

<220>
<221> CDS
<222> (1)...(612)

<400> 3
atg gcg cac tcg cgc agc cac cac cac ctc ctc ctg ctc ccc gcg ccc 48
Met Ala His Ser Arg Ser His His His Leu Leu Leu Leu Pro Ala Pro
1 5 10 15
atg gcc acg gcg tgc ttg ctc ctc gcc acc ctc ctc gcg ctc tgc gcc 96
Met Ala Thr Ala Cys Leu Leu Leu Ala Thr Leu Leu Ala Leu Cys Ala
20 25 30
gcg ccg gcg ccg acc cac ggc gcg cgc gtc ctc atg ccg ggc ggc gcg 144
Ala Pro Ala Pro Thr His Gly Ala Arg Val Leu Met Pro Gly Gly Ala
35 40 45
ggc gcg gtg acc aag gcg cag cag ggt ggc acc ggc agc ggc agc aac 192
Gly Ala Val Thr Lys Ala Gln Gln Gly Gly Thr Gly Ser Gly Ser Asn
50 55 60
gcg acg gcg gac gag tac ctg gcg ccg cac aac cag gcg cgc gcg gcg 240
Ala Thr Ala Asp Glu Tyr Leu Ala Pro His Asn Gln Ala Arg Ala Ala
65 70 75 80
gtg ggc gtg gcc ccg ctg cgg tgg aac gcg ggc ctg gct tcg gcg gcc 288
Val Gly Val Ala Pro Leu Arg Trp Asn Ala Gly Leu Ala Ser Ala Ala
85 90 95
gcg ggg acg gtg gcg cag cag cgg cgg cag ggc ggg tgc gcg ttc gcg 336
Ala Gly Thr Val Ala Gln Gln Arg Arg Gln Gly Gly Cys Ala Phe Ala
100 105 110
gac gtg ggg gcc agc ccc tac ggc gcg aac cag ggg tgg gcg agc tac 384
Asp Val Gly Ala Ser Pro Tyr Gly Ala Asn Gln Gly Trp Ala Ser Tyr
115 120 125
cgc gcg cgc ccc gcc gag gtg gtg gcg ctg tgg gtg gcg gag ggg cgg 432
Arg Ala Arg Pro Ala Glu Val Val Ala Leu Trp Val Ala Glu Gly Arg
130 135 140
tac tac acc cac gcc aac aac acg tgc gcc gcg ggg cgg cag tgc ggc 480
Tyr Tyr Thr His Ala Asn Asn Thr Cys Ala Ala Gly Arg Gln Cys Gly
145 150 155 160
acg tac acg cag gtg gtg tgg cgc aac acc gcc gag gtc ggg tgc gcg 528
Thr Tyr Thr Gln Val Val Trp Arg Asn Thr Ala Glu Val Gly Cys Ala

165										170					175					
cag	gcc	agc	tgc	gcc	acg	ggc	gcc	acg	ctc	acg	ctc	tgc	ctg	tac	aac		576			
Gln	Ala	Ser	Cys	Ala	Thr	Gly	Ala	Thr	Leu	Thr	Leu	Cys	Leu	Tyr	Asn					
			180					185					190							
ccg	cac	ggc	aac	gtg	cag	ggc	cag	agc	ccc	tac	tag						612			
Pro	His	Gly	Asn	Val	Gln	Gly	Gln	Ser	Pro	Tyr	*									
		195					200													